

SEQUENCE LISTING



<110> TAKAGI, MASARU
HIRATSU, KEIICHIROU

<120> GENE AND PEPTIDE FOR TRANSCRIPTIONAL REPRESSOR

<130> 036910-0111

<140> 10/500,361

<141> 2004-06-28

<150> PCT/JP02/13443

<151> 2002-12-24

<150> JP 2001-395487

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<150> JP 2001-395488

<151> 2001-12-26

<150> JP 2002-160671

<151> 2002-05-31

<160> 148

<170> PatentIn Ver. 3.3

<210> 1

<211> 12

<212> PRT

<213> Nicotiana tabacum

<400> 1

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1 5 10

<210> 2

<211> 41

<212> DNA

<213> Nicotiana tabacum

<400> 2

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41

<210> 3

<211> 45

<212> DNA

<213> Nicotiana tabacum

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45

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

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Leu Asp Leu Asn Leu Ala Pro Pro Met Glu Phe
1 5 10

<210> 5
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic nucleotide sequence

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<210> 6
<211> 42
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic nucleotide sequence

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<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

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Leu Asp Leu Asn Leu Ala Ala Ala Ala Ala
1 5 10

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<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

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<213> Arabidopsis thaliana

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<210> 11
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<400> 13
Leu Asp Leu Asn Leu
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<212> PRT
<213> Arabidopsis thaliana

<400> 16
Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala
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<213> Arabidopsis thaliana

<400> 17
cctggatcta gaactccggt tgggtttcgc ttaag 35

<210> 18
<211> 39
<212> DNA
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<400> 18
tcgacttaag cgaaacccaa acggagttct agatccagg 39

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<212> PRT
<213> Arabidopsis thaliana

<400> 19
Leu Asp Leu Glu Leu Gly Phe Ala
1 5

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1 5 10

<210> 23
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<400> 23
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<210> 24
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<400> 24
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<210> 25
<211> 65
<212> DNA
<213> Cauliflower mosaic virus

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cgctg 65

<210> 26
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<212> DNA
<213> Cauliflower mosaic virus

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atcta 65

<210> 27
<211> 24
<212> DNA
<213> Cauliflower mosaic virus

<400> 27
cgccaggggt ttccagtcg cgac 24

<210> 28
<211> 37
<212> DNA
<213> Cauliflower mosaic virus

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aagggtaacg ttaaggatag tgggattgtg cgtcatc 37

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<213> Arabidopsis thaliana

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<210> 30
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<212> DNA
<213> Arabidopsis thaliana

<400> 30
gataaagtta ttaccgtcga cttagcgaa ac 32

<210> 31
<211> 204
<212> PRT

<213> Arabidopsis thaliana

<400> 31

Met Glu Arg Ser Asn Ser Ile Glu Leu Arg Asn Ser Phe Tyr Gly Arg
1 5 10 15

Ala Arg Thr Ser Pro Trp Ser Tyr Gly Asp Tyr Asp Asn Cys Gln Gln
20 25 30

Asp His Asp Tyr Leu Leu Gly Phe Ser Trp Pro Pro Arg Ser Tyr Thr
35 40 45

Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala Leu Gly Gly
50 55 60

His Met Asn Val His Arg Arg Asp Arg Ala Arg Leu Arg Leu Gln Gln
65 70 75 80

Ser Pro Ser Ser Ser Ser Thr Pro Ser Pro Pro Tyr Pro Asn Pro Asn
85 90 95

Tyr Ser Tyr Ser Thr Met Ala Asn Ser Pro Pro Pro His His Ser Pro
100 105 110

Leu Thr Leu Phe Pro Thr Leu Ser Pro Pro Ser Ser Pro Arg Tyr Arg
115 120 125

Ala Gly Leu Ile Arg Ser Leu Ser Pro Lys Ser Lys His Thr Pro Glu
130 135 140

Asn Ala Cys Lys Thr Lys Lys Ser Ser Leu Leu Val Glu Ala Gly Glu
145 150 155 160

Ala Thr Arg Phe Thr Ser Lys Asp Ala Cys Lys Ile Leu Arg Asn Asp
165 170 175

Glu Ile Ile Ser Leu Glu Leu Glu Ile Gly Leu Ile Asn Glu Ser Glu
180 185 190

Gln Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala
195 200

<210> 32

<211> 18

<212> DNA

<213> Arabidopsis thaliana

<400> 32

gaatgatgaa atcatcag

18

<210> 33

<211> 29

<212> DNA

<213> Arabidopsis thaliana

<400> 33
catggcgact cctaacgaag tatctgcac 29

<210> 34
<211> 39
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<213> Arabidopsis thaliana

<400> 34
atcgttcaaa aactcaaggc taactaatca acaacggtc 39

<210> 35
<211> 65
<212> DNA
<213> Cauliflower mosaic virus

<400> 35
agcttagatc tgcaagacc cttctctata taaggaagt catttcatt ggagaggaca 60
cgctg 65

<210> 36
<211> 65
<212> DNA
<213> Cauliflower mosaic virus

<400> 36
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atcta 65

<210> 37
<211> 24
<212> DNA
<213> Cauliflower mosaic virus

<400> 37
cgccagggtt ttccagtcg cgac 24

<210> 38
<211> 37
<212> DNA
<213> Cauliflower mosaic virus

<400> 38
aagggttaagc ttaaggatag tgggattgtg cgtcatc 37

<210> 39
<211> 44
<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 39

gatcagccgc cgatcagccg ccgatcagcc gccgatcagc cgcc 44

<210> 40

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 40

ctagggcggc tgatcggcgg ctgatcggcg gctgatcggc cggct 45

<210> 41

<211> 76

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 41

gatccacaat taccaacaac aacaacaac aaacaacatt acaattacag atcccggggg 60
taccgtgcac gagctc 76

<210> 42

<211> 70

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 42

cgctgacggt acccccgga tctgtaattg taatgttgtt tgtgttgtt 60
ggtaattgtg 70

<210> 43

<211> 21

<212> DNA

<213> Arabidopsis thaliana

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<400> 44 atgaatcccc gggatattat tc	22
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<400> 45 cgacactgca gatcacaac	19
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<210> 47 <211> 24 <212> DNA <213> Nicotiana tabacum	
<400> 47 agtgggtcct actgtgtcgg actc	24
<210> 48 <211> 39 <212> DNA <213> Nicotiana tabacum	
<400> 48 ccaaataaca ttatcggtcg actcaaaatt ccataggtg	39
<210> 49 <211> 35 <212> PRT <213> Nicotiana tabacum	
<400> 49 Val Gly Pro Thr Val Ser Asp Ser Ser Ser Ala Val Glu Glu Asn Gln	

1 5 10 15

Tyr Asp Gly Lys Arg Asp Ile Ala Leu Ala Leu Asn Leu Ala Pro Pro
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Met Glu Phe
35

<210> 50

<211> 111

<212> DNA

<213> Nicotiana tabacum

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aaagaggaat tgatcttgat cttaaccttg ctccacctat ggaatttga g 111

<210> 51

<211> 116

<212> DNA

<213> Nicotiana tabacum

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catcatattg gtctcttcc actgcagagg acgagtccga cacagtagga cccact 116

<210> 52

<211> 1887

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1887)

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1 5 10 15

tct gga tca ctt ggt gaa gtt gat ttc tgt cct gtt cca caa gct gag 96
Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu
20 25 30

cct gat tcc att gtt gaa gat gac tat act gat gat gag att gat gtt 144
Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val
35 40 45

gat gaa ttg gag agg agg atg tgg aga gac aaa atg cgg ctt aaa cgt 192
Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
50 55 60

ctc aag gag cag gat aag ggt aaa gaa ggt gtt gat gct gct aaa cag 240

Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln
65 70 75 80

agg cag tct caa gag caa gct agg agg aag aaa atg tct aga gct caa 288
Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
85 90 95

gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa gct 336
Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala
100 105 110

caa ggc ttt gtt tat ggg att att ccg gag aat ggg aag cct gtg act 384
Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
115 120 125

ggg gct tct gat aat tta agg gag tgg tgg aaa gat aag gtt agg ttt 432
Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe
130 135 140

gat cgt aat ggt cct gcg gct att acc aag tat caa gcg gag aat aat 480
Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn
145 150 155 160

atc ccg ggg att cat gaa ggt aat aac ccg att gga ccg act cct cat 528
Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
165 170 175

acc ttg caa gag ctt caa gac acg act ctt gga tcg ctt ttg tct gcg 576
Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala
180 185 190

ttg atg caa cac tgt gat cct cct cag aga cgt ttt cct ttg gag aaa 624
Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys
195 200 205

gga gtt cct cct ccg tgg tgg cct aat ggg aaa gag gat tgg tgg cct 672
Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro
210 215 220

caa ctt ggt ttg cct aaa gat caa ggt cct gca cct tac aag aag cct 720
Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro
225 230 235 240

cat gat ttg aag aag gcg tgg aaa gtc ggc gtt ttg act gcg gtt atc 768
His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
245 250 255

aag cat atg ttt cct gat att gct aag atc cgt aag ctc gtg agg caa 816
Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
260 265 270

tct aaa tgt ttg cag gat aag atg act gct aaa gag agt gct acc tgg 864
Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
275 280 285

ctt gct att att aac caa gaa gag tcc ttg gct aga gag ctt tat ccc 912

Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro
290 295 300

gag tca tgt cca cct ctt tct ctg tct ggt gga agt tgc tcg ctt ctg 960
Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
305 310 315 320

atg aat gat tgc agt caa tac gat gtt gaa ggt ttc gag aag gag tct 1008
Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser
325 330 335

cac tat gaa gtg gaa gag ctc aag cca gaa aaa gtt atg aat tct tca 1056
His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser
340 345 350

aac ttt ggg atg gtt gct aaa atg cat gac ttt cct gtc aaa gaa gaa 1104
Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu
355 360 365

gtc cca gca gga aac tcg gaa ttc atg aga aag aga aag cca aac aga 1152
Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg
370 375 380

gat ctg aac act att atg gac aga acc gtt ttc acc tgc gag aat ctt 1200
Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu
385 390 395 400

ggg tgt gcg cac agc gaa atc agc cgg gga ttt ctg gat agg aat tcg 1248
Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser
405 410 415

aga gac aac cat caa ctg gca tgt cca cat cga gac agt cgc tta ccg 1296
Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro
420 425 430

tat gga gca gca cca tcc agg ttt cat gtc aat gaa gtt aag cct gta 1344
Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val
435 440 445

gtt gga ttt cct cag cca agg cca gtg aac tca gta gcc caa cca att 1392
Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile
450 455 460

gac tta acg ggt ata gtt cct gaa gat gga cag aag atg atc tca gag 1440
Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu
465 470 475 480

ctc atg tcc atg tac gac aga aat gtc cag agc aac caa acc tct atg 1488
Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met
485 490 495

gtc atg gaa aat caa agc gtg tca ctg ctt caa ccc aca gtc cat aac 1536
Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn
500 505 510

cat caa gaa cat ctc cag ttc cca gga aac atg gtg gaa gga agt ttc 1584

His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe
515 520 525

ttt gaa gac ttg aac atc cca aac aga gca aac aac aac agc agc 1632
Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Ser Ser
530 535 540

aac aat caa acg ttt ttt caa ggg aac aac aac aac aat gtg ttt 1680
Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Val Phe
545 550 555 560

aag ttc gac act gca gat cac aac aac ttt gaa gct gca cat aac aac 1728
Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
565 570 575

aac aat aac agt agc ggc aac agg ttc cag ctt gtg ttt gat tcc aca 1776
Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
580 585 590

ccg ttc gac atg gcg tca ttc gat tac aga gat gat atg tcg atg cca 1824
Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro
595 600 605

gga gta gta gga acg atg gat gga atg cag cag aag cag caa gat gta 1872
Gly Val Val Gly Thr Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val
610 615 620

tcc ata tgg ttc taa 1887
Ser Ile Trp Phe
625

<210> 53
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<212> DNA
<213> Nicotiana tabacum

<220>
<221> CDS
<222> (1)..(678)

<400> 53
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Met Ala Val Lys Asn Lys Val Ser Asn Gly Asn Leu Lys Gly Gly Asn
1 5 10 15

gtg aaa aca gat gga gtt aag gag gtt cac tac aga ggt gta agg aag 96
Val Lys Thr Asp Gly Val Lys Glu Val His Tyr Arg Gly Val Arg Lys
20 25 30

agg cca tgg ggt cgg tat gca gct gaa atc cgt gac ccg ggt aag aag 144
Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Gly Lys Lys
35 40 45

agt cgg gtc tgg tta ggt act ttc gac acg gcg gaa gag gcg gct aag 192
 Ser Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Lys
 50 55 60

gcg tac gac acc gcc gct cga gag ttt cgt gga ccc aaa gca aaa act 240
 Ala Tyr Asp Thr Ala Ala Arg Glu Phe Arg Gly Pro Lys Ala Lys Thr
 65 70 75 80

aac ttc cct tca ccg acg gag aat cag agc cca agt cac agc agc acc 288
 Asn Phe Pro Ser Pro Thr Glu Asn Gln Ser Pro Ser His Ser Ser Thr
 85 90 95

gtg gag tcc tct agt gga gag aat ggt gtt cac gcg ccg cct cat gcg 336
 Val Glu Ser Ser Ser Gly Glu Asn Gly Val His Ala Pro Pro His Ala
 100 105 110

ccg ctc gag ctg gat ctc acg cgc cgt ctt ggc tcc gtt gct gca gat 384
 Pro Leu Glu Leu Asp Leu Thr Arg Arg Leu Gly Ser Val Ala Ala Asp
 115 120 125

ggc ggt gac aac tgt cgc cgt tct ggg gaa gtt ggg tac ccg att ttc 432
 Gly Gly Asp Asn Cys Arg Arg Ser Gly Glu Val Gly Tyr Pro Ile Phe
 130 135 140

cac cag cag ccg act gtg gcg gtt ctg cca aat ggc cag ccg gtt ctg 480
 His Gln Gln Pro Thr Val Ala Val Leu Pro Asn Gly Gln Pro Val Leu
 145 150 155 160

ctc ttt gat tct ttg tgg cgg gcg gga gtt gtt aac agg cct cag cct 528
 Leu Phe Asp Ser Leu Trp Arg Ala Gly Val Val Asn Arg Pro Gln Pro
 165 170 175

tac cat gta acg ccg atg ggg ttt aac ggc gtt aac gcc gga gtg ggt 576
 Tyr His Val Thr Pro Met Gly Phe Asn Gly Val Asn Ala Gly Val Gly
 180 185 190

cct act gtg tcg gac tcg tcc tct gca gtg gaa gag aac caa tat gat 624
 Pro Thr Val Ser Asp Ser Ser Ser Ala Val Glu Glu Asn Gln Tyr Asp
 195 200 205

ggg aaa aga gga att gat ctt gat ctt aac ctt gct cca cct atg gaa 672
 Gly Lys Arg Gly Ile Asp Leu Asp Leu Asn Leu Ala Pro Pro Met Glu
 210 215 220

ttt tga 678
 Phe
 225

<210> 54
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 <213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(933)

<400> 54

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Met Asp Val Asp Val Phe Asn Gly Trp Gly Arg Pro Arg Phe Glu Asp
1 5 10 15

gaa tcc ctt atg cca cct ggg ttt agg ttt cat cca act gat gaa gag 96
Glu Ser Leu Met Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu
20 25 30

ctg atc act tac tat ctc ctc aag aag gtt ctt gac tct aat ttc tct 144
Leu Ile Thr Tyr Tyr Leu Leu Lys Lys Val Leu Asp Ser Asn Phe Ser
35 40 45

tgt gcc gcc att tct caa gtt gat ctc aac aag tct gag cct tgg gag 192
Cys Ala Ala Ile Ser Gln Val Asp Leu Asn Lys Ser Glu Pro Trp Glu
50 55 60

ctt cct gag aaa gcg aaa atg ggg gag aag gag tgg tac ttc ttc aca 240
Leu Pro Glu Lys Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Thr
65 70 75 80

cta aga gac cgt aaa tac cca acg gga ctg aga acg aac aga gca aca 288
Leu Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr
85 90 95

gaa gct ggt tac tgg aaa gcc act ggt aaa gac aga gag atc aaa agc 336
Glu Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Arg Glu Ile Lys Ser
100 105 110

tca aag aca aaa tca ctt ctc ggg atg aag aaa act ctt gtc ttt tac 384
Ser Lys Thr Lys Ser Leu Leu Gly Met Lys Lys Thr Leu Val Phe Tyr
115 120 125

aaa ggc aga gct cct aaa gga gag aag agt tgt tgg gtc atg cat gag 432
Lys Gly Arg Ala Pro Lys Gly Glu Lys Ser Cys Trp Val Met His Glu
130 135 140

tat cgc ctt gac ggc aaa ttc tct tac cat tac att tcc tcc tcc gct 480
Tyr Arg Leu Asp Gly Lys Phe Ser Tyr His Tyr Ile Ser Ser Ser Ala
145 150 155 160

aag gat gaa tgg gtt ctc tgt aaa gtt tgt ctg aaa agc ggc gta gtt 528
Lys Asp Glu Trp Val Leu Cys Lys Val Cys Leu Lys Ser Gly Val Val
165 170 175

agt aga gag acg aac ttg atc tct tct tct tct tct gcc gtc acc 576
Ser Arg Glu Thr Asn Leu Ile Ser Ser Ser Ser Ser Ala Val Thr
180 185 190

gga gag ttc tcc tct gcc ggt tct gca att gct ccg atc atc aat acc 624
Gly Glu Phe Ser Ser Ala Gly Ser Ala Ile Ala Pro Ile Ile Asn Thr
195 200 205

ttt gcg acg gag cac gtg tcc tgt ttc tcc aat aac tct gct gct cat 672
Phe Ala Thr Glu His Val Ser Cys Phe Ser Asn Asn Ser Ala Ala His
210 215 220

acc gat gcg agc ttt cat aca ttc ctt ccc gct cca ccg ccg tca ctg 720
Thr Asp Ala Ser Phe His Thr Phe Leu Pro Ala Pro Pro Pro Ser Leu
225 230 235 240

ccc cca cgt cag cca cgt cac gtc ggt gat ggc gtg gcg ttt ggt cag 768
Pro Pro Arg Gln Pro Arg His Val Gly Asp Gly Val Ala Phe Gly Gln
245 250 255

ttt ctg gat ttg gga tca tcg gga cag att gat ttc gat gca gca gca 816
Phe Leu Asp Leu Gly Ser Ser Gly Gln Ile Asp Phe Asp Ala Ala Ala
260 265 270

gca gcg ttc ttt ccg aat cta cct tct ctg cct ccc acg gtt ctt cct 864
Ala Ala Phe Phe Pro Asn Leu Pro Ser Leu Pro Pro Thr Val Leu Pro
275 280 285

cct cct ccg tca ttt gca atg tac ggt gga ggc tcc ccc gcc gtg agt 912
Pro Pro Pro Ser Phe Ala Met Tyr Gly Gly Gly Ser Pro Ala Val Ser
290 295 300

gtg tgg ccg ttt act ctc tga 933
Val Trp Pro Phe Thr Leu
305 310

<210> 55
<211> 60
<212> DNA
<213> Arabidopsis thaliana

<400> 55
ttaagcgaaa cccaaacgga gttctagatc cagatcgaga gtaaagggcc acacactcac 60

<210> 56
<211> 26
<212> DNA
<213> Arabidopsis thaliana

<400> 56
gggatggatg ttgatgtgtt taacgg 26

<210> 57
<211> 34
<212> DNA
<213> Arabidopsis thaliana

<400> 57

cctggatcta gaactccgtt tgggttcgc ttaa 34

<210> 58
<211> 39
<212> DNA
<213> Arabidopsis thaliana

<400> 58
tcgacttaag cgaaacccaa acggagttct agatccagg 39

<210> 59
<211> 37
<212> DNA
<213> Arabidopsis thaliana

<400> 59
ccttgatctt aacctgctc cacctatgga atttga 37

<210> 60
<211> 42
<212> DNA
<213> Arabidopsis thaliana

<400> 60
tcgactcaaa attccatagg tggagcaagg ttaagatcaa gg 42

<210> 61
<211> 30
<212> PRT
<213> Arabidopsis thaliana

<400> 61
Asn Asp Glu Ile Ile Ser Leu Glu Leu Glu Ile Gly Leu Ile Asn Glu
1 5 10 15

Ser Glu Gln Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala
20 25 30

<210> 62
<211> 35
<212> DNA
<213> Arabidopsis thaliana

<400> 62
aaaatggagg gttcgtccaa agggctgcga aaagg 35

<210> 63
<211> 34
<212> DNA
<213> Arabidopsis thaliana

<400> 63
atcaaatttc acagtctctc catcgaaaag actc 34

<210> 64
<211> 40
<212> DNA
<213> Arabidopsis thaliana

<400> 64
ctggatctgg atctagaact ccggttggt ttcgcttaag 40

<210> 65
<211> 40
<212> DNA
<213> Arabidopsis thaliana

<400> 65
cttaagcgaa acccaaacgg agttctagat ccagatccag 40

<210> 66
<211> 747
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(747)

<400> 66
atg gag ggt tgc tcc aaa ggg ctg cga aaa ggt gct tgg act act gaa 48
Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Thr Glu
1 5 10 15

gaa gat agt ctc ttg aga cag tgc att aat aag tat gga gaa ggc aaa 96
Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys
20 25 30

tgg cac caa gtt cct gta aga gct ggg cta aac cgg tgc agg aaa agt 144
Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
35 40 45

tgt aga tta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga 192
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50 55 60

aaa ctt agc tct gat gaa gtc gat ctt ctt ctt cgc ctt cat agg ctt 240
Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu
65 70 75 80

cta ggg aat agg tgg tct tta att gct gga aga tta cct ggt cgg acc 288
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95

gca aat gac gtc aag aat tac tgg aac act cat ctg agt aag aaa cat 336
 Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
 100 105 110

gaa ccg tgt tgt aag ata aag atg aaa aag aga gac att acg ccc att 384
 Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile
 115 120 125

cct aca aca ccg gca cta aaa aac aat gtt tat aag cct cga cct cga 432
 Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg
 130 135 140

tcc ttc aca gtt aac aac gac tgc aac cat ctc aat gcc cca cca aaa 480
 Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys
 145 150 155 160

gtt gac gtt aat cct cca tgc ctt gga ctt aac atc aat aat gtt tgt 528
 Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys
 165 170 175

gac aat agt atc ata tac aac aaa gat aag aag aaa gac caa cta gtg 576
 Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val
 180 185 190

aat aat ttg att gat gga gat aat atg tgg tta gag aaa ttc cta gag 624
 Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Glu
 195 200 205

gaa agc caa gag gta gat att ttg gtt cct gaa gcg acg aca aca gaa 672
 Glu Ser Gln Glu Val Asp Ile Leu Val Pro Glu Ala Thr Thr Thr Glu
 210 215 220

aag ggg gac acc ttg gct ttt gac gtt gat caa ctt tgg agt ctt ttc 720
 Lys Gly Asp Thr Leu Ala Phe Asp Val Asp Gln Leu Trp Ser Leu Phe
 225 230 235 240

gat gga gag act gtg aaa ttt gat tag 747
 Asp Gly Glu Thr Val Lys Phe Asp
 245

<210> 67
 <211> 34
 <212> DNA
 <213> Arabidopsis thaliana

<400> 67
 aaaatgagaa tgacaagaga tggaaaagaa catg 34

<210> 68
 <211> 34
 <212> DNA

<213> Arabidopsis thaliana

<400> 68

aaggcaatac ccattagtaa aatccatcat agtg

34

<210> 69

<211> 660

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(660)

<400> 69

atg aga atg aca aga gat gga aaa gaa cat gaa tac aag aaa ggt tta 48

Met Arg Met Thr Arg Asp Gly Lys Glu His Glu Tyr Lys Lys Gly Leu

1 5 10 15

tgg aca gtt gaa gaa gac aag atc ctc atg gat tat gtc cga act cat 96

Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr Val Arg Thr His

20 25 30

ggc cag ggc cac tgg aac cgc atc gcc aag aaa act ggg ctc aag aga 144

Gly Gln Gly His Trp Asn Arg Ile Ala Lys Lys Thr Gly Leu Lys Arg

35 40 45

tgt ggg aaa agc tgt agg ttg aga tgg atg aac tac tta agc cct aat 192

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn

50 55 60

gtt aac aga ggc aat ttt act gac caa gaa gaa gat ctc atc atc aga 240

Val Asn Arg Gly Asn Phe Thr Asp Gln Glu Glu Asp Leu Ile Ile Arg

65 70 75 80

ctc cac aag ctc ctc ggc aac aga tgg tgg ttg ata gcg aaa aga gtt 288

Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val

85 90 95

ccg gga aga aca gac aac caa gta aag aat tac tgg aac aca cat ctc 336

Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu

100 105 110

agc aag aaa ctt ggt ctc gga gat cat tca act gcc gtc aaa gcc gca 384

Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala

115 120 125

tgc ggt gta gag tct cca ccg tct atg gcc ctt ata acc aca acg tcc 432

Cys Gly Val Glu Ser Pro Pro Ser Met Ala Leu Ile Thr Thr Thr Ser

130 135 140

tcc tct cat caa gag atc tcc ggt gga aaa aat tca act cta agg ttc 480

Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe

145 150 155 160

gac act tta gtt gac gaa tcc aaa ctc aaa cca aaa tcc aaa cta gtc 528
Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val
165 170 175

cac gca aca cca act gac gta gaa gtt gca gct acg gtt cca aat ctg 576
His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu
180 185 190

ttc gat acc ttt tgg gtt ctt gaa gac gac ttc gag ctt agt tca ctc 624
Phe Asp Thr Phe Trp Val Leu Glu Asp Asp Phe Glu Leu Ser Ser Leu
195 200 205

act atg atg gat ttt act aat ggg tat tgc ctt tga 660
Thr Met Met Asp Phe Thr Asn Gly Tyr Cys Leu
210 215

<210> 70
<211> 24
<212> DNA
<213> Arabidopsis thaliana

<400> 70
cgtggatcac agcaatacag agcc 24

<210> 71
<211> 25
<212> DNA
<213> Arabidopsis thaliana

<400> 71
cctcctgcac ttccacttcg tcttc .25

<210> 72
<211> 20
<212> DNA
<213> Arabidopsis thaliana

<400> 72
aaaaagatga caggatgggt 20

<210> 73
<211> 20
<212> DNA
<213> Arabidopsis thaliana

<400> 73
cccctgttc tgtcttgta 20

<210> 74

<211> 26
<212> DNA
<213> Arabidopsis thaliana

<400> 74
gggatggata attcagctcc agattc 26

<210> 75
<211> 22
<212> DNA
<213> Arabidopsis thaliana

<400> 75
aactctaagg agctgcattt tg 22

<210> 76
<211> 33
<212> DNA
<213> Arabidopsis thaliana

<400> 76
gggatgagaa taaggagaag agatgaaaaa gag 33

<210> 77
<211> 33
<212> DNA
<213> Arabidopsis thaliana

<400> 77
aaggcagtac tcaatatcac tagaagcaaa att 33

<210> 78
<211> 33
<212> DNA
<213> Arabidopsis thaliana

<400> 78
atggccgtcg acatgtottc caaacaaccc acc 33

<210> 79
<211> 30
<212> DNA
<213> Arabidopsis thaliana

<400> 79
gcagggagtt ctctgccgt tcttgaatag 30

<210> 80
<211> 11
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 80

Leu Glu Leu Arg Leu Ala Ala Ala Ala Ala
1 5 10

<210> 81

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide sequence

<400> 81

actagaactc cgttggctg ccgcagcggc tgcataatga g 41

<210> 82

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide sequence

<400> 82

tcgactcatt atgcagccgc tgcggcagcc aaacggagtt ctagt 45

<210> 83

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 83

Asp Leu Glu Leu Arg Leu
1 5

<210> 84

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 84

agatctagaa ctccgtttgt aatgag

26

<210> 85

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 85

tcgactcatt acaaacggag ttctagatct

30

<210> 86

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 86

Leu Asp Leu Gln Leu Arg Leu Gly Tyr Tyr

1

5

10

<210> 87

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 87

actggatcta caactccgtt tgggttatta ctaatgag

38

<210> 88

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 88
tcgactcatt agtaataacc caaacggagt ttagatcca g 41

<210> 89
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 89
Leu Asp Leu Glu Leu Arg Leu
1 5

<210> 90
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 90
actggatcta gaactccgtt tgtaatgag 29

<210> 91
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 91
tcgactcatt acaaacggag ttctagatcc agt 33

<210> 92
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 92
Leu Asp Leu Glu Leu Ala Ala Ala Ala Ala

1 5 10

<210> 93
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 93
actggatcta gaactcgctg cgcagcggc tgcataatga g 41

<210> 94
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 94
tcgactcatt atgcagccgc tgcggcagcg agttctagat ccagt 45

<210> 95
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 95
Leu Asp Leu Glu Leu Arg Leu Ala Ala Ala
1 5 10

<210> 96
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 96
actggatcta gaactccgtt tggctgccgc ataattgag 38

<210> 97
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 97
tcgactcatt atgcggcagc caaacggagt tctagatcca gt 42

<210> 98
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 98
Leu Glu Leu Asp Leu Ala Ala Ala Ala Ala
1 5 10

<210> 99
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 99
ccttgagctt gatcttgctg ctgctgctgc tgcttgag 38

<210> 100
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 100
tcgactcaag cagcagcagc agcagcaaga tcaagctcaa gg 42

<210> 101
<211> 8
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 101

Leu Asp Leu Glu Leu Arg Leu Gly
1 5

<210> 102

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide sequence

<400> 102

cctggatcta gaactccgtg gttaag 26

<210> 103

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide sequence

<400> 103

tcgacttaac cacggagttc tagatccagg 30

<210> 104

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 104

Leu Glu Leu Arg Leu
1 5

<210> 105

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 105

tctagaactc cgtttgtaat gag 23

<210> 106

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 106

tcgactcatt acaaacggag ttctaga 27

<210> 107

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 107

Phe Asp Leu Asn Phe Ala Pro Leu Asp Cys Val
1 5 10

<210> 108

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 108

attcgatctt aattttgcac cgttggttg tgtttaag 38

<210> 109

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 109
tcgactcatt aaacacaatc caacgggtgca aaattaagat cgaat 45

<210> 110
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 110
Phe Asp Leu Asn Ile Phe Pro Pro Ile Pro Glu Phe
1 5 10

<210> 111
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 111
gtttgacctc aacatccctc cgatccctga attctaag 38

<210> 112
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 112
tcgacttaga attcagggat cggaggggatg ttgaggtcaa ac 42

<210> 113
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 113
Phe Gln Phe Asp Leu Asn Phe Pro Pro Leu Asp Cys Val

1 5 10

<210> 114
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 114
cttcaattc gatctaatt ttccaccgtt ggattgtgtt taag 44

<210> 115
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 115
tcgactaaa cacaatccaa cgggtggaaaa ttaagatcga attgaaag 48

<210> 116
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 116
Asp Leu Asp Leu Arg Leu
1 5

<210> 117
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 117
actggatcta gatctccgtt tgtaatgag 29

<210> 118
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence

<400> 118
tcgactcatt acaaacggag atctagatcc agt 33

<210> 119
<211> 11
<212> PRT
<213> Arabidopsis thaliana

<400> 119
Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala
1 5 10

<210> 120
<211> 12
<212> PRT
<213> Arabidopsis thaliana

<400> 120
Leu Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala
1 5 10

<210> 121
<211> 19
<212> PRT
<213> Arabidopsis thaliana

<400> 121
Val Ser Val Trp Pro Phe Thr Leu Asp Leu Asp Leu Glu Leu Arg Leu
1 5 10 15

Gly Phe Ala

<210> 122
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide motif

<220>

<221> MOD_RES
<222> (1)
<223> Leu or Phe

<220>
<221> MOD_RES
<222> (5)
<223> Leu or Phe

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<220>
<221> MOD_RES
<222> (6)
<223> Any amino acid
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<400> 122
Xaa Asp Leu Asn Xaa Xaa Pro
1 5

<210> 123
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

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<220>
<221> MOD_RES
<222> (1)..(10)
<223> This region may encompass 0-10 variable amino
      acids
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<220>
<221> MOD_RES
<222> (14)
<223> Asn or Glu

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<220>  
<221> MOD_RES  
<222> (16)..(21)  
<223> Any amino acid
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<400> 123

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Asp Leu Xaa Leu Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

<210> 124
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (1)..(10)

<223> This region may encompass 0-10 variable amino acids

<220>

<221> MOD_RES

<222> (15)

<223> Phe or Ile

<220>

<221> MOD_RES

<222> (16)..(21)

<223> Any amino acid

<400> 124

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Asp Leu Asn Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

<210> 125

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (1)..(3)

<223> This region may be Leu, Asp-Leu, or Leu-Asp-Leu

<220>

<221> MOD_RES

<222> (6)

<223> Glu, Gln, or Asp

<220>

<221> MOD_RES

<222> (10)..(19)

<223> This region may encompass 0-10 variable amino acids

<400> 125

Xaa Xaa Xaa Asp Leu Xaa Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1 5 10 15

Xaa Xaa Xaa

<210> 126
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (3)
<223> Glu, Gln, or Asp

<400> 126
Asp Leu Xaa Leu Arg Leu
1 5

<210> 127
<211> 5
<212> PRT
<213> Arabidopsis thaliana

<400> 127
Leu Asp Leu Glu Leu
1 5

<210> 128
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (4)
<223> Asn or Glu

<400> 128
Leu Asp Leu Xaa Leu
1 5

<210> 129
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (5)
<223> Phe or Ile

<400> 129
Phe Asp Leu Asn Xaa
1 5

<210> 130
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (3)
<223> Glu, Gln, or Asp

<400> 130
Asp Leu Xaa Leu Arg Leu
1 5

<210> 131
<211> 615
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(615)

<400> 131
atg gag aga tca aac agc ata gag ttg agg aac agc ttc tat ggc cgt 48
Met Glu Arg Ser Asn Ser Ile Glu Leu Arg Asn Ser Phe Tyr Gly Arg
1 5 10 15

gca aga act tca cca tgg agc tat gga gat tat gat aat tgc caa cag 96
Ala Arg Thr Ser Pro Trp Ser Tyr Gly Asp Tyr Asp Asn Cys Gln Gln
20 25 30

gat cat gat tat ctt cta ggg ttt tca tgg cca cca aga tcc tac act 144
Asp His Asp Tyr Leu Leu Gly Phe Ser Trp Pro Pro Arg Ser Tyr Thr

35 40 45
 tgc agc ttc tgc aaa agg gaa ttc aga tcg gct caa gca ctt ggt ggc 192
 Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala Leu Gly Gly
 50 55 60
 cac atg aat gtt cac aga aga gac aga gca aga ctc aga tta caa cag 240
 His Met Asn Val His Arg Arg Asp Arg Ala Arg Leu Arg Leu Gln Gln
 65 70 75 80
 tct cca tca tca tct tca aca cct tct cct cct tac cct aac cct aat 288
 Ser Pro Ser Ser Ser Thr Pro Ser Pro Pro Tyr Pro Asn Pro Asn
 85 90 95
 tac tct tac tca acc atg gca aac tct cct cct cct cat cat tct cct 336
 Tyr Ser Tyr Ser Thr Met Ala Asn Ser Pro Pro Pro His His Ser Pro
 100 105 110
 cta acc cta ttt cca acc ctt tct cct cca tcc tca cca aga tat agg 384
 Leu Thr Leu Phe Pro Thr Leu Ser Pro Pro Ser Ser Pro Arg Tyr Arg
 115 120 125
 gca ggt ttg atc cgt tcc ttg agc ccc aag tca aaa cat aca cca gaa 432
 Ala Gly Leu Ile Arg Ser Leu Ser Pro Lys Ser Lys His Thr Pro Glu
 130 135 140
 aac gct tgt aag act aag aaa tca tct ctt tta gtg gag gct gga gag 480
 Asn Ala Cys Lys Thr Lys Lys Ser Ser Leu Leu Val Glu Ala Gly Glu
 145 150 155 160
 gct aca agg ttc acc agt aaa gat gct tgc aag atc ctg agg aat gat 528
 Ala Thr Arg Phe Thr Ser Lys Asp Ala Cys Lys Ile Leu Arg Asn Asp
 165 170 175
 gaa atc atc agc ttg gag ctt gag att ggt ttg att aac gaa tca gag 576
 Glu Ile Ile Ser Leu Glu Leu Glu Ile Gly Leu Ile Asn Glu Ser Glu
 180 185 190
 caa gat ctg gat cta gaa ctc cgt ttg ggt ttc gct taa 615
 Gln Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe Ala
 195 200

<210> 132
 <211> 628
 <212> PRT
 <213> Arabidopsis thaliana

<400> 132
 Met Met Phe Asn Glu Met Gly Met Cys Gly Asn Met Asp Phe Phe Ser
 1 5 10 15
 Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu
 20 25 30

Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val
 35 40 45

Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
 50 55 60

Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln
 65 70 75 80

Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
 85 90 95

Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala
 100 105 110

Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
 115 120 125

Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe
 130 135 140

Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn
 145 150 155 160

Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
 165 170 175

Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala
 180 185 190

Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys
 195 200 205

Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro
 210 215 220

Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro
 225 230 235 240

His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
 245 250 255

Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
 260 265 270

Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
 275 280 285

Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro
 290 295 300

Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
 305 310 315 320

Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser

325	330	335
His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser		
340	345	350
Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu		
355	360	365
Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg		
370	375	380
Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu		
385	390	395
Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser		
405	410	415
Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro		
420	425	430
Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val		
435	440	445
Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile		
450	455	460
Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu		
465	470	475
Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met		
485	490	495
Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn		
500	505	510
His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe		
515	520	525
Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser		
530	535	540
Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Val Phe		
545	550	555
Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn		
565	570	575
Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr		
580	585	590
Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro		
595	600	605
Gly Val Val Gly Thr Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val		
610	615	620

Ser Ile Trp Phe
625

<210> 133
<211> 225
<212> PRT
<213> *Nicotiana tabacum*

<400> 133
Met Ala Val Lys Asn Lys Val Ser Asn Gly Asn Leu Lys Gly Gly Asn
1 5 10 15
Val Lys Thr Asp Gly Val Lys Glu Val His Tyr Arg Gly Val Arg Lys
20 25 30
Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Gly Lys Lys
35 40 45
Ser Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Lys
50 55 60
Ala Tyr Asp Thr Ala Ala Arg Glu Phe Arg Gly Pro Lys Ala Lys Thr
65 70 75 80
Asn Phe Pro Ser Pro Thr Glu Asn Gln Ser Pro Ser His Ser Ser Thr
85 90 95
Val Glu Ser Ser Ser Gly Glu Asn Gly Val His Ala Pro Pro His Ala
100 105 110
Pro Leu Glu Leu Asp Leu Thr Arg Arg Leu Gly Ser Val Ala Ala Asp
115 120 125
Gly Gly Asp Asn Cys Arg Arg Ser Gly Glu Val Gly Tyr Pro Ile Phe
130 135 140
His Gln Gln Pro Thr Val Ala Val Leu Pro Asn Gly Gln Pro Val Leu
145 150 155 160
Leu Phe Asp Ser Leu Trp Arg Ala Gly Val Val Asn Arg Pro Gln Pro
165 170 175
Tyr His Val Thr Pro Met Gly Phe Asn Gly Val Asn Ala Gly Val Gly
180 185 190
Pro Thr Val Ser Asp Ser Ser Ser Ala Val Glu Glu Asn Gln Tyr Asp
195 200 205
Gly Lys Arg Gly Ile Asp Leu Asp Leu Asn Leu Ala Pro Pro Met Glu
210 215 220

Phe
225

<210> 134
<211> 310
<212> PRT
<213> Arabidopsis thaliana

<400> 134
Met Asp Val Asp Val Phe Asn Gly Trp Gly Arg Pro Arg Phe Glu Asp
1 5 10 15

Glu Ser Leu Met Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu
20 25 30

Leu Ile Thr Tyr Tyr Leu Leu Lys Lys Val Leu Asp Ser Asn Phe Ser
35 40 45

Cys Ala Ala Ile Ser Gln Val Asp Leu Asn Lys Ser Glu Pro Trp Glu
50 55 60

Leu Pro Glu Lys Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Thr
65 70 75 80

Leu Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr
85 90 95

Glu Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Arg Glu Ile Lys Ser
100 105 110

Ser Lys Thr Lys Ser Leu Leu Gly Met Lys Lys Thr Leu Val Phe Tyr
115 120 125

Lys Gly Arg Ala Pro Lys Gly Glu Lys Ser Cys Trp Val Met His Glu
130 135 140

Tyr Arg Leu Asp Gly Lys Phe Ser Tyr His Tyr Ile Ser Ser Ser Ala
145 150 155 160

Lys Asp Glu Trp Val Leu Cys Lys Val Cys Leu Lys Ser Gly Val Val
165 170 175

Ser Arg Glu Thr Asn Leu Ile Ser Ser Ser Ser Ser Ala Val Thr
180 185 190

Gly Glu Phe Ser Ser Ala Gly Ser Ala Ile Ala Pro Ile Ile Asn Thr
195 200 205

Phe Ala Thr Glu His Val Ser Cys Phe Ser Asn Asn Ser Ala Ala His
210 215 220

Thr Asp Ala Ser Phe His Thr Phe Leu Pro Ala Pro Pro Pro Ser Leu
225 230 235 240

Pro Pro Arg Gln Pro Arg His Val Gly Asp Gly Val Ala Phe Gly Gln
245 250 255

Phe Leu Asp Leu Gly Ser Ser Gly Gln Ile Asp Phe Asp Ala Ala Ala
260 265 270

Ala Ala Phe Phe Pro Asn Leu Pro Ser Leu Pro Pro Thr Val Leu Pro
275 280 285

Pro Pro Pro Ser Phe Ala Met Tyr Gly Gly Gly Ser Pro Ala Val Ser
290 295 300

Val Trp Pro Phe Thr Leu
305 310

<210> 135
<211> 248
<212> PRT
<213> Arabidopsis thaliana

<400> 135
Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Thr Glu
1 5 10 15

Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys
20 25 30

Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50 55 60

Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100 105 110

Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile
115 120 125

Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg
130 135 140

Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys
145 150 155 160

Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys
165 170 175

Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val
180 185 190

Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Glu
195 200 205

Glu Ser Gln Glu Val Asp Ile Leu Val Pro Glu Ala Thr Thr Thr Glu
210 215 220

Lys Gly Asp Thr Leu Ala Phe Asp Val Asp Gln Leu Trp Ser Leu Phe
225 230 235 240

Asp Gly Glu Thr Val Lys Phe Asp
245

<210> 136

<211> 219

<212> PRT

<213> Arabidopsis thaliana

<400> 136

Met Arg Met Thr Arg Asp Gly Lys Glu His Glu Tyr Lys Lys Gly Leu
1 5 10 15

Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr Val Arg Thr His
20 25 30

Gly Gln Gly His Trp Asn Arg Ile Ala Lys Lys Thr Gly Leu Lys Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn
50 55 60

Val Asn Arg Gly Asn Phe Thr Asp Gln Glu Glu Asp Leu Ile Ile Arg
65 70 75 80

Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val
85 90 95

Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu
100 105 110

Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala
115 120 125

Cys Gly Val Glu Ser Pro Pro Ser Met Ala Leu Ile Thr Thr Thr Ser
130 135 140

Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe
145 150 155 160

Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val
165 170 175

His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu
180 185 190

Phe Asp Thr Phe Trp Val Leu Glu Asp Asp Phe Glu Leu Ser Ser Leu
195 200 205

Thr Met Met Asp Phe Thr Asn Gly Tyr Cys Leu
210 215

<210> 137
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (7)..(16)
<223> This region may encompass 0 to 10 variable amino
acid residues

<400> 137
Asp Leu Glu Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

<210> 138
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (8)..(17)
<223> This region may encompass 0 to 10 variable amino
acid residues

<400> 138
Leu Asp Leu Glu Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa

<210> 139
<211> 18
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>

<221> MOD_RES

<222> (9)..(18)

<223> This region may encompass 0 to 10 variable amino
acid residues

<400> 139

Asp Leu Asp Leu Glu Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa

<210> 140

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>

<221> MOD_RES

<222> (10)..(19)

<223> This region may encompass 0 to 10 variable amino
acid residues

<400> 140

Leu Asp Leu Asp Leu Glu Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa

<210> 141

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>

<221> MOD_RES

<222> (7)..(16)

<223> This region may encompass 0 to 10 variable amino
acid residues

<400> 141
Asp Leu Gln Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

<210> 142
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (8)..(17)
<223> This region may encompass 0 to 10 variable amino
acid residues

<400> 142
Leu Asp Leu Gln Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa

<210> 143
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (9)..(18)
<223> This region may encompass 0 to 10 variable amino
acid residues

<400> 143
Asp Leu Asp Leu Gln Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa

<210> 144
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (10)..(19)

<223> This region may encompass 0 to 10 variable amino acid residues

<400> 144

Leu Asp Leu Asp Leu Gln Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa

<210> 145

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (7)..(16)

<223> This region may encompass 0 to 10 variable amino acid residues

<400> 145

Asp Leu Asp Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

<210> 146

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (8)..(17)

<223> This region may encompass 0 to 10 variable amino acid residues

<400> 146

Leu Asp Leu Asp Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1 5 10 15

Xaa

<210> 147
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (9)..(18)
<223> This region may encompass 0 to 10 variable amino
acid residues

<400> 147
Asp Leu Asp Leu Asp Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa

<210> 148
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (10)..(19)
<223> This region may encompass 0 to 10 variable amino
acid residues

<400> 148
Leu Asp Leu Asp Leu Asp Leu Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa